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OM protein - protein search, using sw model

Run on: March 12, 2005, 09:17:03 ; Search time 163 Seconds
(without alignments)
14.237 Million cell updates/sec

Title: US-10-099-895-4

Perfect score: 32

Sequence: 1 HSRSLP 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing filter 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneeqp19808:*\n2: geneeqp19908:*\n3: geneeqp20005:*\n4: geneeqp20018:*\n5: geneeqp20028:*\n6: geneeqp20038:*\n7: geneeqp20038:*\n8: geneeqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	32	100.0	6 4 AAU00347	AAU00347 Binding m
2	32	100.0	15 4 AAU00378	AAU00378 Beta-c pe
3	32	100.0	46 4 ABG04731	ABG04731 Novel hum
4	32	100.0	166 8 ADQ66566	ADQ66566 Novel hum
5	32	100.0	294 4 ABH11968	ABH11968 Human juv
6	32	100.0	294 4 AAM79974	AAM79974 Human pro
7	32	100.0	374 8 ABOS8506	ABOS8506 Human gen
8	32	100.0	433 8 AAM76411	AAM76411 Human bet
9	32	100.0	471 8 ADJ48911	ADJ48911 OIL-asso
10	32	100.0	897 4 AAR20982	AAR20982 Sequence
11	32	100.0	897 4 AAU00387	AAU00387 Cytokine
12	32	100.0	897 4 AAU00388	AAU00388 Cytokine
13	32	100.0	897 4 AAU00385	AAU00385 Cytokine
14	32	100.0	897 4 AAU00374	AAU00374 Cytokine
15	32	100.0	897 8 ADM67207	ADM67207 Human adi
16	32	100.0	897 8 ADRE6990	ADRE6990 Human can
17	32	100.0	897 8 ADQ39970	ADQ39970 Human can
18	32	100.0	897 8 ADQ39971	ADQ39971 Human myo
19	32	100.0	903 8 ADQ39972	ADQ39972 Human myo
20	32	100.0	1688 7 ADJ70893	ADJ70893 Human hea
21	30	93.8	15 2 AAM93974	AAM93974 Human IRS
22	30	93.8	114 5 ADK35491	ADK35491 Novel hum
23	30	93.8	119 7 ABOT1202	ABOT1202 Pseudomon
24	30	93.8	137 2 AAR79067	AAR79067 Mouse Fas
25	30	93.8	138 2 AAR79068	AAR79068 Mouse Fas

26	30	93.8	143 3 AAB08266	AAB08266 Amino aci
27	30	93.8	179 2 AAR79069	AAR79069 Mouse Fas
28	30	93.8	278 8 ADJ36209	ADJ36209 Self-coal
29	30	93.8	279 2 AAR77282	AAR77282 Mouse Fas
30	30	93.8	279 2 AAR79098	AAR79098 Mouse Fas
31	30	93.8	279 2 AAR88357	AAR88357 Mouse Fas
32	30	93.8	279 8 ADJ63978	ADJ63978 Human Fas
33	30	93.8	279 8 ADJ71818	ADJ71818 Human Fas
34	30	93.8	279 8 ADN07589	ADN07589 Human Fas
35	30	93.8	318 8 ADJ36253	ADJ36253 Self-coal
36	30	93.8	331 4 ABG23914	ABG23914 Novel hum
37	30	93.8	436 4 ABG15961	ABG15961 Novel hum
38	30	93.8	1155 2 AAR28047	AAR28047 IRS-1 pro
39	30	93.8	1231 8 ADN98331	ADN98331 Mouse ins
40	30	93.8	1235 6 AA016354	AA016354 Rat IRSAL
41	30	93.8	1242 2 AAY13461	AAY13461 Amino aci
42	30	93.8	1242 2 AAM93972	AAM93972 Human IRS
43	30	93.8	1242 4 AAB83921	AAB83921 Amino aci
44	30	93.8	1242 6 ABB99797	ABB99797 Amino aci
45	30	93.8	1242 6 ABG72369	ABG72369 Human ins

ALIGNMENTS

RESULT 1
AAU00347 standard, peptide; 6 AA.

AAU00347; 04-JUL-2001 (first entry)

Binding motif #1 used in study of receptor binding motifs.

Common Beta chain; Beta-c; binding motif; cancer; therapeutic;
acute myeloid leukaemia; AML; inflammatory disease; asthma;
rheumatoid arthritis; cell proliferative disease.

OS Synthetic.

Key Location/Qualifiers
Modified-site 4 /note="Optionally phosphorylated"

WO200119847-A1.

22-MAR-2001.

15-SEP-2000; 2000WO-AU001118.

15-SEP-1999; 99AU-00002875.

12-JUL-2000; 2000AU-00008733.

(MEDV-) MEDVET SCI PTY LTD.

(BERN-) BERNDT M C.

Guthridge MA, Stomski FC, Lopez AF;

WPI; 2001-244778/25.

New binding motif of a receptor capable of binding to cytoplasmic protein, for use as a tool for treating and preventing cell proliferative diseases such as acute myeloid leukemia and cancer.

Claim 8; Page 60; 101p; English.

The sequence represents the amino acid sequence of binding motif #1 used in study of a binding motif (I) of a receptor capable of binding a cytoplasmic protein. (I) comprises an amino acid sequence in which at least one amino acid is serine/threonine. An antagonist to the interaction of (I) to a cytoplasmic protein is useful as a cancer therapeutic, especially for preventing or treating leukemia such as

CC acute myeloid leukemia (AML), and inflammatory diseases e.g., asthma and
CC rheumatoid arthritis, and for preventing functions related to cell
CC activation. The interaction of (I) and cytoplasmic protein is useful as a
CC tool for treating and preventing cell proliferative diseases such as AML
CC and cancer
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 32; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSRSLP 6
AC |||||
DB 1 HSRSLP 6

RESULT 2

ID AAU00378 standard; peptide; 15 AA.

AC AAU00378;

DT 04-JUL-2001 (first entry)

DE Beta-c peptide #1 used in study of a receptor binding motif.

XX Common Beta chain; Beta-c; binding motif; cancer; therapeutic;

KW acute myeloid leukemia; AML; inflammatory disease; asthma;

KM rheumatoid arthritis; cell proliferative disease.

XX Synthetic.

FX Key Location/Qualifiers
FT Modified-site 9 /note="Optionally phosphorylated"

PN WO200119847-A1.

PD 22-MAR-2001.

PF 15-SEP-2000; 2000WO-AU001118.

PR 15-SEP-1999; 99AU-00002875.

PR 12-JUL-2000; 2000AU-00008733.

PA (MEDV-) MEDVET SCI PTY LTD.

PI (BERNDT) BERNDT M C.

PI Guthridge MA, Stomski PC, Lopez AF,

DR WPI; 2001-244778/25.

XX New binding motif of a receptor capable of binding to cytoplasmic

PT protein, for use as a tool for treating and preventing cell proliferative

PT diseases such as acute myeloid leukemia and cancer.

PS Disclosure; Fig 7; 101pp; English.

XX The sequence represents the amino acid sequence of Beta-c peptide #1 used

CC in the study of a binding motif (I) of a receptor capable of binding a

CC cytoplasmic protein. (I) comprises an amino acid sequence in which at

CC least one amino acid is serine/threonine. An antagonist to the

CC interaction of (I) to a cytoplasmic protein is useful as a cancer

CC therapeutic, especially for preventing or treating leukemia such as

CC acute myeloid leukemia (AML), and inflammatory diseases e.g., asthma and

CC rheumatoid arthritis, and for preventing functions related to cell

CC activation. The interaction of (I) and cytoplasmic protein is useful as a

CC tool for treating and preventing cell proliferative diseases such as AML

CC and cancer
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 32; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSRSLP 6
AC |||||
DB 6 HSRSLP 11

RESULT 3
ID ABG04731 standard; protein; 46 AA.

AC ABG04731;

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #4722.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US008631.

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

PA (HYSE-) HYSEQ INC.

PI Dmanac RT, Liu C, Tang YT,

DR WPI; 2001-639362/73.

XX N-PSDB; AAS68918.

XX Claim 20; SEQ ID NO 35090; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)

CC sequences. (I) is useful as hybridization probes, polymerase chain

CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

CC and in recombinant production of (II). The polynucleotides are also used

CC in diagnostics as expressed sequence tags for identifying expressed

CC genes. (I) is useful in gene therapy techniques to restore normal

CC activity of (II) or to treat disease states involving (II). (II) is

CC useful for generating antibodies against it, detecting or quantitating a

CC polypeptide in tissue, as molecular weight markers and as a food

CC supplement. (II) and its binding partners are useful in medical imaging

CC of sites expressing (II). (I) and (II) are useful for treating disorders

CC involving aberrant protein expression or biological activity. The

CC polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. ABG00010-ABG030377 represent novel human diagnostic

CC amino acid sequences of the invention. Note: The sequence data for this

CC patent did not appear in the printed Specification, but was obtained in

CC electronic format directly from WIPO at

CC ftp://wipo.int/pub/published_pct_sequences
XX
SQ Sequence 46 AA;

Query Match 100.0%; Score 32; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 11;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HSRSLP 6
 |||||
 XX 6 HSRSLP 11

Db

RESULT 4
 ADO66566
 ID ADO66566 standard; protein; 166 AA.

AC ADO66566;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Novel human protein sequence #1539.

KM osteopathic; neuroprotective; nootropic; antiparkinsonian; cyostatic;
 KM gene therapy; diagnostic marker; morbid state; osteoporosis;
 KM neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
 KM cancer.

OS Homo sapiens.
 XX
 PN EP1440981-A2.
 XX
 PD 28-JUL-2004.
 XX
 PF 21-JAN-2004; 2004EP-00001196.
 XX
 PR 21-JAN-2003; 2003JP-00102206.
 PR 09-MAY-2003; 2003JP-00131392.
 XX
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.

PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Nagai K, Irie R;
 XX
 DR MPI: 2004-535376/52.
 DR N-PSDB; ADO64378.

XX
 PT Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
 PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
 XX
 PS Claim 1; SEQ ID NO 3727; 2449bp; English.

CC The invention relates to 2495 novel polynucleotides (I) and their encoded
 CC polypeptides, sequences hybridizing to these nucleotides, sequences
 CC encoding partial polypeptides and sequences having 70% or 90% identity to
 CC the nucleotide and protein sequences. The nucleotides and polypeptides
 CC are useful as diagnostic markers or therapeutic target for the diseases
 CC or morbid states. They are also useful for treating osteoporosis,
 CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
 CC dementia and various cancers. This sequence corresponds to a protein
 CC sequence of the invention.

XX
 SEQ Sequence 166 AA;

Query Match 100.0%; Score 32; DB 8; Length 166;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HSRSLP 6
 |||||
 Db 30 HSRSLP 35

RESULT 5
 ABB11968
 ID ABB11968 standard; peptide; 294 AA.
 XX
 AC ABB11968;
 XX

DT 11-JAN-2002 (first entry)
 XX
 DE Human juvenile hormone esterase binding protein homologue, SEQ:2338.
 XX
 KM Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KM haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KM inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
 KM proliferation; metastasis; cancer; tumor; haematopoietic disorder;
 KM myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KM chronic inflammatory condition; proliferative retinopathy;
 KM atherosclerosis; coronary heart disease; arterial ischaemia;
 KM bone disorder; osteoporosis; vascular growth disorder;
 KM tissue regeneration; wound healing; infection; immune disorder;
 KM cell culture; drug screening; gene therapy; antiinflammatory;
 KM antiasthmatic; antiarthritis; haemostatic; antiatherosclerotic;
 KM cyostatic; osteopathic; vasotropic; cardiac; virucide; antibacterial;
 KM antifungal; vulnary; antitumor.

OS Homo sapiens.
 XX
 PD WO200157188-A2.
 XX
 PN 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US003800.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YF, Liu C, Drmanac RT;
 PI MPI: 2001-457740/49.
 XX
 DR N-PSDB; ABA09212.

XX
 PT Human proteins and DNA encoding sequences useful for preventing, treating
 PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
 PT and cancer.
 XX
 PS Claim 20; Page 288; 1963bp; English.

XX
 CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to

CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a novel human
CC polypeptide of the invention
XX

SQ Sequence 294 AA;

Query Match 100.0%; Score 32; DB 4; Length 294;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HSRSLP 6
Db 16 HSRSLP 21

RESULT 6
AAM79974
ID AAM79974 standard; protein, 294 AA.
XX
AC AAM79974;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 3620.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KM tissue growth factor; immunomodulatory; cancer; leukaemia;
KM nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001MO-US004098.

XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.

XX (HYSE-) HYSEQ INC.
XX

PI Tang YF, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y,
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW,
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX

DR WPI; 2001-476283/51.
DR N-PSDB; AAKS3107.
XX

PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX

PS Claim 20; Page 400; 6221pp; English.
XX

CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM79323-AAM80102) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or

CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX

SQ Sequence 294 AA;

Query Match 100.0%; Score 32; DB 4; Length 294;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HSRSLP 6
Db 16 HSRSLP 21

RESULT 7
ABO58506
ID ABO58506 standard; protein, 374 AA.
XX
AC ABO58506;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human genome derived single exon protein #4740.

XX Human; gene expression; single exon probe; microarray;
KM alternative splicing event; genomic alteration.
XX
OS Homo sapiens.
XX
PN US2003194704-A1.
XX
PD 16-OCT-2003.
XX
PF 03-APR-2002; 2002US-00029386.
XX
PR 03-APR-2002; 2002US-00029386.

XX (PENN/) PENN S G.
XX (RANK/) RANK D R.
XX (HANZ/) HANZEL D K.
XX
PI Penn SG, Rank DR, Hanzel DK;
XX
DR WPI; 2004-119264/12.
XX

PT New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.
XX

PS Claim 45; SEQ ID NO 32140; 80pp; English.
XX

CC The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and
CC encoding at least 8 amino acids of any of the 688 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridises under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing

CC human gene expression data by subcription, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above. The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterizing
 CC alternative splicing events, in detecting and characterizing gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe protein of the invention. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docid=20030194704

CC Sequence 374 AA;

Query Match 100.0%; Score 32; DB 8; Length 374;

Best Local Similarity 100.0%; Pred. No. 93;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HRSRSLP 6
 |||||
 Db 75 HRSRSLP 80

RESULT 8
 AAW76411
 ID AAW76411 standard; peptide; 433 AA.

AC AAW76411;

DT 20-JAN-1999 (first entry)

DE Human betac cytoplasmic domain amino acid sequence.

XX JAK2 protein; cytoplasmic domain; betac subunit; screening; asthma;
 KW interleukin; granulocyte macrophage-colony stimulating factor; GM-CSF;
 KW IL-3; IL-5; human.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Domain 7..68 /note= "JAK2 activation domain; claimed for in claim 1"

FT Region 9..17 /note= "BOX 1 region"

FT Region 69..74 /note= "BOX 2 region"

FT Domain 180..355 /note= "Ras/MAPK activation domain"

FT MO9843087-A1.

PN 01-OCT-1998.

PF 23-MAR-1998; 98WO-US005387.

PR 24-MAR-1997; 97US-0041511P.

PA (PHMA) PHARMACIA & UPJOHN CO.

PI Roberde SL, Kayes PS;

DR WPI; 1998-532151/45.

DR N-PSDB; AAV61795.

XX Screening for compounds useful for preventing or treating asthma - by
 PT determining if compounds inhibit binding of the JAK2 protein to e.g. IL-
 PT 3, IL-5 or GM-CSF.

PS Disclosure; Fig 5A-D; 112pp; English.

XX This represents the amino acid sequence of the human betac cytoplasmic
 CC domain. A JAK2 protein activating fragment of this betac subunit can be
 CC used in the method of the invention of screening for compounds useful for
 CC treating or preventing asthma. The method comprises contacting a molecule
 CC comprising at least the N-terminal 294 amino acid residues of the JAK2
 CC protein, with another molecule comprising at least 13 membrane-proximal
 CC cytoplasmic amino acids of interleukin (IL)-3, IL-5 or granulocyte
 CC macrophage-colony stimulating factor (GM-CSF) proteins in the presence of
 CC the candidate compound, and determining whether the first and the second
 CC molecules form a complex. If the compound inhibits complex formation, it
 CC can be used to treat asthma

SO Sequence 433 AA;

Query Match 100.0%; Score 32; DB 2; Length 433;

Best Local Similarity 100.0%; Pred. No. 1,1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HRSRSLP 6
 |||||
 Db 134 HRSRSLP 139

RESULT 9
 ADJ48911
 ID ADJ48911 standard; protein; 471 AA.

AC ADJ48911;

DT 06-MAY-2004 (first entry)

DE Oil-associated gene related protein #411.

XX oil-associated gene; transgenic; enhanced seed oil; vegetable oil.

OS Unidentified.

PN US2004025202-A1.

PD 05-FEB-2004.

PF 14-MAR-2003; 2003US-00389566.

PR 15-MAR-2002; 2002US-0365301P.

PR 26-JUN-2002; 2002US-0391786P.

PR 26-JUN-2002; 2002US-0392018P.

PA (LAUR/) LAURIE C. C.

PA (SAVA/) SAVAGE T. T.

PA (LEDE/) LEDEAUX J. R.

PA (ROGE/) ROGERS J. A.

PI Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;

DR WPI; 2004-142683/14.

PT Novel recombinant DNA construct comprising a promoter functional in

PT plants operably linked to an oil-associated gene for producing transgenic

PT plant seed.

PS Example 3; SEQ ID NO 915; 22pp; English.

XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in plants operably linked to an oil-associated gene.
 CC The construct is useful for transgenic plant seed which has in its genome
 CC the construct, that is functional, in the plant to transcribe the oil-
 CC associated gene. The transgenic plant seed grows into a plant having
 CC enhanced seed oil as compared to wild type. The construct is useful for
 CC producing hybrid maize seed. The transgenic plant seed is useful for
 CC producing vegetable oil. The present sequence represents the amino acid

CC sequence of an oil-associated gene related protein.
 XX
 SQ Sequence 471 AA;

Query Match 100.0%; Score 32; DB 8; Length 471;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HSRSLP 6
 |||||
 DB 361 HSRSLP 366

RESULT 10

AAR20982
 ID AAR20982 standard; protein; 897 AA.

AC AAR20982;

DT 17-MAY-1992 (first entry)

DE Sequence of beta-chain of a human granulocyte-macrophage colony
 DE stimulating factor (GM-CSF) receptor.

KW Agonist; antagonist; myeloid leukaemia; therapy; screening; diagnosis;
 KW granulocyte-macrophage colony stimulating factor.

XX Homo sapiens.

Key Location/Qualifiers

FT Peptide 1..17

FT Modified-site 58..60

FT Modified-site 191..193

FT Modified-site 346..348

FT Modified-site /label= as above

PN WO9201788-A.

XX 06-FEB-1992.

PF 18-JUL-1990; 90US-00554745.

PR 18-JUL-1990; 90US-00554745.

PS (SCHE) SCHERING CORP.

PI Hayashida K, Kitamura T, Miyajima A;

DR WPI; 1992-064947/08.

DR N-PSDB; AAQ21453.

PT Beta-chain of human granulocyte-macrophage CSF receptor - used for
 PT screening agonists and antagonists of human GM-CSF, e.g. for diagnosing
 PT myeloid leukaemia.

PS Claim 2; Page 15-18; 26pp; English.

CC The nucleic acid encoding the human GM-CSF beta-chain is isolated from a
 CC cDNA library prepd. from poly(A)⁺ RNA from TF-1 cells. The high affinity
 CC human GM-CSF receptor (Kd < 1 nM) can be used for screening candidate GM-
 CC CSF agonists and antagonists e.g. for treating myeloid leukemias

XX Sequence 897 AA;

Query Match 100.0%; Score 32; DB 2; Length 897;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HSRSLP 6
 |||||

DB 598 HSRSLP 603

RESULT 11

AAU00387
 ID AAU00387 standard; protein; 897 AA.

AC AAU00387;

DT 04-JUL-2001 (first entry)

DE Cytokine receptor common beta chain precursor, CYRB, mutant #4.

KW Cytokine receptor common beta chain precursor; binding motif; cancer;
 KW therapeutic; acute myeloid leukaemia; AML; inflammatory disease; asthma;
 KW rheumatoid arthritis; cell proliferative disease; CYRB; human; mutant;

XX Homo sapiens.

OS Synthetic.

Key Location/Qualifiers

FT MISC-difference 585 /note= "Wild-type Ser substituted by Ala"

PN WO200119847-A1.

PD 22-MAR-2001.

PF 15-SEP-2000; 2000WO-AU001118.

PR 15-SEP-1999; 99AU-00002875.

PR 12-JUL-2000; 2000AU-00008733.

PA (MEDV-) MEDVET SCI PTY LTD.

PA (BERN/) BERNDT M C.

PI Guthridge MA, Stomski FC, Lopez AF;

DR WPI; 2001-244778/25.

PT New binding motif of a receptor capable of binding to cytoplasmic
 PT protein, for use as a tool for treating and preventing cell proliferative
 PT diseases such as acute myeloid leukemia and cancer.

XX Example 10; Page; 101pp; English.

CC The sequence represents the amino acid sequence of cytokine receptor
 CC common beta chain precursor, CYRB, mutant #4, used in study of a binding
 CC motif (I) of a receptor capable of binding a cytoplasmic protein. (I)
 CC comprises an amino acid sequence in which at least one amino acid is
 CC serine/threonine. An antagonist to the interaction of (I) to a
 CC cytoplasmic protein is useful as a cancer therapeutic, especially for
 CC preventing or treating leukemia such as acute myeloid leukemia (AML),
 CC and inflammatory diseases e.g., asthma and rheumatoid arthritis, and for
 CC preventing functions related to cell activation. The interaction of (I)
 CC and cytoplasmic protein is useful as a tool for treating and preventing
 CC cell proliferative diseases such as AML and cancer. Note: The present
 CC sequence is not shown in the specification but is derived from the wild-
 CC type human common beta chain precursor sequence given in Figure 1 (see
 CC AAU00374)

XX Sequence 897 AA;

Query Match 100.0%; Score 32; DB 4; Length 897;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HSRSLP 6
 |||||

DB 598 HSRSLP 603

```

RESULT 12
AAU00388
ID AAU00388 standard; protein; 897 AA.
XX
AC AAU00388;
XX
DT 04-JUL-2001 (first entry)
XX
DE Cytokine receptor common beta chain precursor, CYRB, mutant #5.
XX
KW Cytokine receptor common beta chain precursor; binding motif; cancer;
KW therapeutic; acute myeloid leukemia; AML; inflammatory disease; asthma;
KW rheumatoid arthritis; cell proliferative disease; CYRB; human; mutant;
KW mucin.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 585
FT /note= "Wild-type Ser substituted by Gly"
XX
PN WO200119847-A1.
XX
PD 22-MAR-2001.
XX
PF 15-SEP-2000; 2000WO-AU001118.
XX
PR 15-SEP-1999; 99AU-00002875.
PR 12-JUL-2000; 2000AU-00008733.
XX
PA (MEDV-) MEDVET SCI PTY LTD.
PA (BERN/) BERNDT M C.
XX
PI Guthridge MA, Stomski FC, Lopez AF;
XX
DR WPI; 2001-244778/25.
XX
PT New binding motif of a receptor capable of binding to cytoplasmic
PT protein, for use as a tool for treating and preventing cell proliferative
PT diseases such as acute myeloid leukemia and cancer.
XX
PS Example 10; Page; 101pp; English.
XX
CC The sequence represents the amino acid sequence of cytokine receptor
CC common beta chain precursor, CYRB, mutant #5, used in study of a binding
CC motif (I) of a receptor capable of binding a cytoplasmic protein. (I)
CC comprises an amino acid sequence in which at least one amino acid is
CC serine/threonine. An antagonist to the interaction of (I) to a
CC cytoplasmic protein is useful as a cancer therapeutic, especially for
CC preventing or treating leukemia such as acute myeloid leukemia (AML),
CC and inflammatory diseases e.g., asthma and rheumatoid arthritis, and for
CC preventing functions related to cell activation. The interaction of (I)
CC and cytoplasmic protein is useful as a tool for treating and preventing
CC cell proliferative diseases such as AML and cancer. Note: The present
CC sequence is not shown in the specification but is derived from the wild-
CC type human common beta chain precursor sequence given in Figure 1 (see
CC AAU00374)
XX
SQ Sequence 897 AA;

```

```

Query Match 100.0%; Score 32; DB 4; Length 897;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 HSRSLP 6
   |||||
DB 598 HSRSLP 603

```

```

RESULT 13
AAU00385
ID AAU00385 standard; protein; 897 AA.

```

```

XX
AC AAU00385;
XX
DT 04-JUL-2001 (first entry)
XX
DE Cytokine receptor common beta chain precursor, CYRB, mutant #2.
XX
KW Cytokine receptor common beta chain precursor; binding motif; cancer;
KW therapeutic; acute myeloid leukemia; AML; inflammatory disease; asthma;
KW rheumatoid arthritis; cell proliferative disease; CYRB; human; mutant;
KW mucin.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 836..842
FT /note= "Wild-type RSKRSP substituted by EFAAAA"
XX
PN WO200119847-A1.
XX
PD 22-MAR-2001.
XX
PF 15-SEP-2000; 2000WO-AU001118.
XX
PR 15-SEP-1999; 99AU-00002875.
PR 12-JUL-2000; 2000AU-00008733.
XX
PA (MEDV-) MEDVET SCI PTY LTD.
PA (BERN/) BERNDT M C.
XX
PI Guthridge MA, Stomski FC, Lopez AF;
XX
DR WPI; 2001-244778/25.
XX
PT New binding motif of a receptor capable of binding to cytoplasmic
PT protein, for use as a tool for treating and preventing cell proliferative
PT diseases such as acute myeloid leukemia and cancer.
XX
PS Example 2; Page; 101pp; English.
XX
CC The sequence represents the amino acid sequence of cytokine receptor
CC common beta chain precursor, CYRB, mutant #2, used in study of a binding
CC motif (I) of a receptor capable of binding a cytoplasmic protein. (I)
CC comprises an amino acid sequence in which at least one amino acid is
CC serine/threonine. An antagonist to the interaction of (I) to a
CC cytoplasmic protein is useful as a cancer therapeutic, especially for
CC preventing or treating leukemia such as acute myeloid leukemia (AML),
CC and inflammatory diseases e.g., asthma and rheumatoid arthritis, and for
CC preventing functions related to cell activation. The interaction of (I)
CC and cytoplasmic protein is useful as a tool for treating and preventing
CC cell proliferative diseases such as AML and cancer. Note: The present
CC sequence is not shown in the specification but is derived from the wild-
CC type human common beta chain precursor sequence given in Figure 1 (see
CC AAU00374)
XX
SQ Sequence 897 AA;

```

```

Query Match 100.0%; Score 32; DB 4; Length 897;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 HSRSLP 6
   |||||
DB 598 HSRSLP 603

```

```

RESULT 14
AAU00374
ID AAU00374 standard; protein; 897 AA.
XX
AC AAU00374;
XX

```

DT 04-JUL-2001 (first entry)
 XX Cytokine receptor common beta chain precursor, CYRB.
 DE
 XX
 XX Cytokine receptor common beta chain precursor; binding motif; cancer;
 KW therapeutic; acute myeloid leukaemia; AML; inflammatory disease; asthma;
 KW rheumatoid arthritis; cell proliferative disease; CYRB; human.
 XX
 OS Homo sapiens.
 PN WO200119847-A1.
 PD
 XX
 PD 22-MAR-2001.
 XX
 PF 15-SEP-2000; 2000WO-AU001118.
 XX
 PR 15-SEP-1999; 99AU-00002875.
 PR 12-JUL-2000; 2000AU-00008733.
 XX
 PA (MEDV-) MEDVET SCI PTY LTD.
 PA (BERN/) BERNDT M C.
 XX
 XX Guthridge MA, Stomski FC, Lopez AF;
 FI
 XX WPI; 2001-244778/25.
 DR
 XX
 PT New binding motif of a receptor capable of binding to cytoplasmic
 PT protein, for use as a tool for treating and preventing cell proliferative
 PT diseases such as acute myeloid leukemia and cancer.
 XX
 PS Disclosure; Fig 1; 101pp; English.
 XX
 CC The sequence represents the amino acid sequence of cytokine receptor
 CC common beta chain precursor, CYRB, used in study of a binding motif (I)
 CC of a receptor capable of binding a cytoplasmic protein. (I) comprises an
 CC amino acid sequence in which at least one amino acid is serine/threonine.
 CC An antagonist to the interaction of (I) to a cytoplasmic protein is
 CC useful as a cancer therapeutic, especially for preventing or treating
 CC leukaemia such as acute myeloid leukaemia (AML), and inflammatory
 CC diseases e.g., asthma and rheumatoid arthritis, and for preventing
 CC functions related to cell activation. The interaction of (I) and
 CC cytoplasmic protein is useful as a tool for treating and preventing cell
 CC proliferative diseases such as AML and cancer
 XX
 SQ Sequence 897 AA;
 Query Match 100.0%; Score 32; DB 4; Length 897;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HSRSLP 6
 Db 598 HSRSLP 603
 RESULT 15
 ADM67207
 ID ADM67207 standard; protein; 897 AA.
 XX
 AC ADM67207;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human adipocyte specific CSF 2 receptor beta 1 protein seqid 561.
 XX
 KW human; adipocyte specific; adipose tissue; anti-obesity;
 KW high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
 KW adipogenesis; hypertension; cardiovascular disease; anorectic;
 KW antidiabetic; hypotensive; CSF 2 receptor beta 1.
 XX
 OS Homo sapiens.
 XX
 PN WO2004011618-A2.

XX
 PD 05-FEB-2004.
 XX
 PF 29-JUL-2003; 2003WO-US033684.
 XX
 PR 29-JUL-2002; 2002US-0398785P.
 PR 12-JUN-2003; 2003US-0478206P.
 XX
 PA (HMG-) HMGNE INC.
 PA
 XX
 PI Chada K, Chouinard R, Ashar H, Sayed AMD;
 XX
 DR WPI; 2004-143846/14.
 DR N-PSDB; ADM66928.
 XX
 PT Identifying adipocyte specific genes, useful for treating obesity or
 PT diabetes, and for identifying drug targets, by differential gene
 PT expression analysis between adipose tissue or stromal vascular tissue of
 PT mice of different genotypes.
 XX
 PS Disclosure; SEQ ID NO 561; 91pp; English.
 XX
 CC This invention relates to a novel method for identifying genes that are
 CC over-expressed in adipose tissue and as such it provides targets for anti-
 CC obesity pharmaceutical compositions. Specifically, it refers to a high
 CC mobility group I-C protein (HMGI-C) that is associated with obesity and
 CC is epistatic to leptin, furthermore, it refers to the ob gene where an
 CC autosomal recessive trait is linked to obesity and diabetes. The present
 CC invention describes performing differential gene expression analysis
 CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
 CC of any two different mice selected from a group consisting of wild-type,
 CC HMGI-C -/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using
 CC this method novel nucleotides and the encoded proteins thereof were
 CC identified that are adipocyte specific, and as such can be used for
 CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
 CC hypertension and cardiovascular disease, as well as screening for
 CC compounds that can modulate or prevent adipogenesis and treat diabetes or
 CC obesity. These compositions exhibit anorectic, antidiabetic and
 CC hypotensive activities. This polypeptide sequence is a human homologue of
 CC a murine adipocyte specific protein sequence of the invention.
 XX
 SQ Sequence 897 AA;
 Query Match 100.0%; Score 32; DB 8; Length 897;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HSRSLP 6
 Db 598 HSRSLP 603

Search completed: March 12, 2005, 09:31:49
 Job time : 165 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 09:26:39 ; Search time 41 Seconds
(without alignments)
10.924 Million cell updates/sec

Title: US-10-099-895-4

Perfect score: 32

Sequence: 1 HSRSLP 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: Issued Patents, AA:*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	100.0	433	US-09-046-158A-2	Sequence 2, Appli
2	32	100.0	897	US-07-960-389-2	Sequence 2, Appli
3	30	93.8	15	US-09-508-691-3	Sequence 3, Appli
4	30	93.8	66	US-09-632-287A-6	Sequence 6, Appli
5	30	93.8	119	US-09-252-991A-19948	Sequence 19, Appli
6	30	93.8	137	US-08-339-214-18	Sequence 18, Appli
7	30	93.8	138	US-08-339-214-20	Sequence 20, Appli
8	30	93.8	179	US-08-339-214-22	Sequence 22, Appli
9	30	93.8	279	US-08-339-214-24	Sequence 24, Appli
10	30	93.8	279	US-08-339-214-32	Sequence 32, Appli
11	30	93.8	279	PCT-US95-00362-5	Sequence 5, Appli
12	30	93.8	1155	US-08-094-948A-29	Sequence 29, Appli
13	30	93.8	1155	PCT-US96-09319-29	Sequence 29, Appli
14	30	93.8	1234	US-08-317-310A-15	Sequence 15, Appli
15	30	93.8	1234	PCT-US95-13041-15	Sequence 15, Appli
16	30	93.8	1242	US-09-508-691-1	Sequence 1, Appli
17	30	93.8	1242	US-09-903-248-5	Sequence 5, Appli
18	30	93.8	1242	US-09-903-199-5	Sequence 5, Appli
19	30	93.8	1242	US-09-903-216-5	Sequence 5, Appli
20	30	93.8	1242	US-09-903-063-5	Sequence 5, Appli
21	30	93.8	1242	US-09-859-604-5	Sequence 5, Appli
22	30	93.8	1243	US-08-557-139-2	Sequence 2, Appli
23	29	90.6	210	US-09-162-184-33	Sequence 33, Appli
24	29	90.6	210	US-09-489-777A-33	Sequence 33, Appli
25	29	90.6	346	US-09-252-991A-21871	Sequence 21871, A
26	29	90.6	406	US-09-252-991A-28102	Sequence 28102, A
27	29	90.6	418	US-09-252-991A-32095	Sequence 32095, A

28	29	90.6	432	US-09-252-991A-21794	Sequence 21794, A
29	29	90.6	513	US-09-107-532A-5261	Sequence 5261, Ap
30	28	87.5	21	US-08-712-212-2	Sequence 2, Appli
31	28	87.5	21	PCT-US95-05160-2	Sequence 2, Appli
32	28	87.5	95	US-08-654-462-8	Sequence 8, Appli
33	28	87.5	110	US-08-017-570-2	Sequence 2, Appli
34	28	87.5	110	US-08-471-426-2	Sequence 2, Appli
35	28	87.5	110	US-09-672-609-13	Sequence 13, Appli
36	28	87.5	110	US-09-672-609-15	Sequence 15, Appli
37	28	87.5	110	US-09-672-609-16	Sequence 16, Appli
38	28	87.5	110	US-09-672-609-17	Sequence 17, Appli
39	28	87.5	110	US-09-025-403A-13	Sequence 13, Appli
40	28	87.5	110	US-09-025-403A-15	Sequence 15, Appli
41	28	87.5	110	US-09-025-403A-16	Sequence 16, Appli
42	28	87.5	110	US-09-025-403A-17	Sequence 17, Appli
43	28	87.5	110	PCT-US94-01709-2	Sequence 2, Appli
44	28	87.5	111	US-08-207-169A-4	Sequence 4, Appli
45	28	87.5	144	US-08-540-804-37	Sequence 37, Appli

ALIGNMENTS

RESULT 1
US-09-046-158A-2
Sequence 2, Application US/09046158A
Patent No. 6187552
GENERAL INFORMATION:
APPLICANT: Robert, Steven L.
APPLICANT: Kayles, Paul S.
TITLE OF INVENTION: METHOD FOR IDENTIFYING INHIBITORS OF
TITLE OF INVENTION: JAK2/CYTOKINE RECEPTOR BINDING
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: Pharmacia & Upjohn Co., Intellectual Property
ADDRESSER: Legal Services
STREET: 301 Henrietta Street
CITY: Kalamazoo
STATE: MI
COUNTRY: USA
ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046.158A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Darnley Jr., James D.
REGISTRATION NUMBER: 33,673
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616/833-2210
TELEFAX: 616/833-8897
TELEX: 224401
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-046-158A-2
Query Match 100.0%; Score 32; DB 3; Length 433;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HSRSLP 6
Db 134 HSRSLP 139

RESULT 2

US-07-960-389-2
; Sequence 2, Application US/07960389
; Patent No. 5705611
; GENERAL INFORMATION:
; APPLICANT: HAYASHIDA, Kasuhiro;
; TITLE OF INVENTION: Human GM-CSF Receptor Component
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Gallopington Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disc
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System Software 7.1
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/960,389
; FILING DATE: 07-JAN-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 554,745
; FILING DATE: 18-JUL-1990
; APPLICATION NUMBER: PCT/US 91/04846
; FILING DATE: 16-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Blasdale, John H. C.
; REGISTRATION NUMBER: 31,895
; REFERENCE/DOCKET NUMBER: DX01430
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 298-2902
; TELEFAX: (908) 298-5388
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 897 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; OTHER INFORMATION: Human GM-CSF receptor; Signal Sequence: -17 to -1; Transmembrane

Query Match 100.0%; Score 32; DB 1; Length 897;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HSRSLP 6
DB 598 HSRSLP 603

RESULT 3

US-09-508-691-3
; Sequence 3, Application US/09508691
; Patent No. 6498139
; GENERAL INFORMATION:
; APPLICANT: YAZAKI, YOSHIO
; APPLICANT: ASANO, TOMOICHIRO
; APPLICANT: KUBO, HIDEO
; APPLICANT: KANDA, AKIRA
; TITLE OF INVENTION: REMEDIES FOR DISEASES CAUSED BY INSULIN RESISTANCE
; FILE REFERENCE: 4895-0019-0PCT
; CURRENT APPLICATION NUMBER: US/09/508,691
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: PCT/JP98/04293
; PRIOR FILING DATE: 1998-09-25

; PRIOR APPLICATION NUMBER: JP9-263719
; PRIOR FILING DATE: 1997-09-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
; NAME/KEY: MOD RES
; LOCATION: (9)...(9)
; OTHER INFORMATION: PHOSPHORYLATION
US-09-508-691-3

Query Match 93.8%; Score 30; DB 4; Length 15;
Best Local Similarity 83.3%; Pred. No. 2.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HSRSLP 6
DB 6 HSRSLP 11

RESULT 4

US-09-632-287A-6
; Sequence 6, Application US/09632287A
; Patent No. 6521422
; GENERAL INFORMATION:
; APPLICANT: Heu, Hailing
; APPLICANT: Wooden, Scott K
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Fhm, A No. 6521422e1 Member of the TNF Ligand Supergene Family
; FILE REFERENCE: 01017/35550A
; CURRENT APPLICATION NUMBER: US/09/632,287A
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mouse
US-09-632-287A-6

Query Match 93.8%; Score 30; DB 4; Length 66;
Best Local Similarity 83.3%; Pred. No. 11;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HSRSLP 6
DB 16 HSRSLP 21

RESULT 5

US-09-252-991A-19948
; Sequence 19948, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19948

LENGTH: 119
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19948

Query Match 93.8%; Score 30; DB 4; Length 119;
Best Local Similarity 83.3%; Pred. No. 21;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSRSLP 6
DB 112 HSRSLP 117

RESULT 6
US-08-339-214-18
Sequence 18, Application US/08339214
Patent No. 6348334
GENERAL INFORMATION:
APPLICANT: Nagata, Shigikazu
APPLICANT: Suda, Takashi
APPLICANT: Takahashi, Tomoniro
APPLICANT: Nakamura, No. 634833410
TITLE OF INVENTION: A Fas Ligand, A Fragment Thereof and DNA
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,214
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-139P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8050
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-339-214-18

Query Match 93.8%; Score 30; DB 3; Length 137;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSRSLP 6
DB 10 HSRSLP 15

RESULT 7
US-08-339-214-20
Sequence 20, Application US/08339214
Patent No. 6348334
GENERAL INFORMATION:
APPLICANT: Nagata, Shigikazu
APPLICANT: Suda, Takashi

APPLICANT: Takahashi, Tomoniro
APPLICANT: Nakamura, No. 634833410
TITLE OF INVENTION: A Fas Ligand, A Fragment Thereof and DNA
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,214
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-139P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8050
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-339-214-20

Query Match 93.8%; Score 30; DB 3; Length 138;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSRSLP 6
DB 11 HSRSLP 16

RESULT 8
US-08-339-214-22
Sequence 22, Application US/08339214
Patent No. 6348334
GENERAL INFORMATION:
APPLICANT: Nagata, Shigikazu
APPLICANT: Suda, Takashi
APPLICANT: Takahashi, Tomoniro
APPLICANT: Nakamura, No. 634833410
TITLE OF INVENTION: A Fas Ligand, A Fragment Thereof and DNA
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,214
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-139P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-339-214-22

Query Match 93.8%; Score 30; DB 3; Length 179;
Best Local Similarity 83.3%; Pred. No. 32;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HRSRIP 6
||||:|
Db 52 HRSRIP 57

RESULT 9
US-08-339-214-24
Sequence 24, Application US/08339214
Patent No. 6348334
GENERAL INFORMATION:
APPLICANT: Nagata, Shigikazu
APPLICANT: Suda, Takashi
APPLICANT: Takahashi, Tomoniro
APPLICANT: Nakamura, No. 634833410
TITLE OF INVENTION: A Fas ligand, A Fragment thereof and DNA
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,214
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-139P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 279 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-339-214-24

Query Match 93.8%; Score 30; DB 3; Length 279;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HRSRIP 6
||||:|

Db 152 HRSRIP 157

RESULT 10
US-08-339-214-32
Sequence 32, Application US/08339214
Patent No. 6348334
GENERAL INFORMATION:
APPLICANT: Nagata, Shigikazu
APPLICANT: Suda, Takashi
APPLICANT: Takahashi, Tomoniro
APPLICANT: Nakamura, No. 634833410
TITLE OF INVENTION: A Fas ligand, A Fragment thereof and DNA
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,214
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-139P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 279 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-339-214-32

Query Match 93.8%; Score 30; DB 3; Length 279;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HRSRIP 6
||||:|
Db 152 HRSRIP 157

RESULT 11
PCT-US95-00362-5
Sequence 5, Application PC/TUS9500362
GENERAL INFORMATION:
APPLICANT: IMMUNEX CORPORATION
TITLE OF INVENTION: Ligand That Binds Fas Antigen
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1

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SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00362
FILING DATE: 06-JAN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/179,138
FILING DATE: 07-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,559
FILING DATE: 01-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Cathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2805-MO
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 279 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-00362-5

Query Match          93.8%; Score 30; DB 5; Length 279;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HRSRSLP 6
DB      152 HRSRSLP 157

RESULT 12
US-08-094-948A-29
Sequence 29, Application US/08094948A
GENERAL INFORMATION:
APPLICANT: Kahn, C. Ronald
APPLICANT: White, Morris F.
APPLICANT: Rothenberg, Paul Louis
TITLE OF INVENTION: INSULIN RECEPTOR SUBSTRATE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSER: Lahive & Cockfield
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/094,948A
FILING DATE: 21-JULY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,982
FILING DATE: 18-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis (PLM)
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: JDP-013DV
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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US-08-094-948A-29
Query Match          93.8%; Score 30; DB 1; Length 1155;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HRSRSLP 6
DB      326 HRSRSLP 331

RESULT 13
PCT-US96-09319-29
Sequence 29, Application PC/TUS9609319
GENERAL INFORMATION:
APPLICANT: Kahn, C. Ronald
APPLICANT: White, Morris F.
APPLICANT: Rothenberg, Paul Louis
TITLE OF INVENTION: INSULIN RECEPTOR SUBSTRATE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSER: Lahive & Cockfield
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09319
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/094,948
FILING DATE: 21-JULY-1993
APPLICATION NUMBER: US 07/643,982
FILING DATE: 18-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis (PLM)
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: JDP-013DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-09319-29

Query Match          93.8%; Score 30; DB 5; Length 1155;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HRSRSLP 6
DB      326 HRSRSLP 331

RESULT 14
US-08-317-310A-15
Sequence 15, Application US/08317310A
Patent No. 5858701
GENERAL INFORMATION:
APPLICANT: WHITE, Morris F.
APPLICANT: SUN, Xiao Jian
APPLICANT: PIERCE, Jacalyn H.
TITLE OF INVENTION: THE IRS FAMILY OF GENES
```

NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,310A
FILING DATE: 03-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: JDP-022
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1234 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-317-310A-15

Query Match 93.8%; Score 30; DB 2; Length 1234;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSRSLP 6
|||:|
Db 366 HSRSLP 371

RESULT 15
PCT-US95-13041-15
Sequence 15, Application PC/TUS9513041
GENERAL INFORMATION:
APPLICANT: WHITE, Morris F.
APPLICANT: SUN, Xiao Jian
APPLICANT: PIERCE, Jacalyn H.
TITLE OF INVENTION: THE IRS FAMILY OF GENES
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13041
FILING DATE: Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/317,310
FILING DATE: 03-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: JDP-022PC

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1234 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
PCT-US95-13041-15

Query Match 93.8%; Score 30; DB 5; Length 1234;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSRSLP 6
|||:|
Db 366 HSRSLP 371

Search completed: March 12, 2005, 09:36:23
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 09:35:00 ; Search time 137 Seconds
(without alignments)
14.446 Million cell updates/sec

Title: US-10-099-895-4

Perfect score: 32

Sequence: 1 HSRSLP 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep.*
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8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubppa/US10D_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubppa/US10D_NEW_PUB.pep.*
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19: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	32	100.0	6	13	US-10-099-895-31
3	32	100.0	7	13	US-10-099-895-35
4	32	100.0	15	13	US-10-099-895-39
5	32	100.0	142	15	US-10-425-114-61894
6	32	100.0	195	16	US-10-767-701-37000
7	32	100.0	278	16	US-10-437-963-113805
8	32	100.0	294	15	US-10-275-774-2338
9	32	100.0	374	14	US-10-029-386-32140
10	32	100.0	459	16	US-10-437-963-117359
11	32	100.0	471	15	US-10-389-566-915
12	32	100.0	897	13	US-10-099-895-1
13	32	100.0	897	17	US-10-741-600-1633

14	32	100.0	897	17	US-10-741-600-1634	Sequence 1634, Ap
15	32	100.0	903	17	US-10-741-600-1635	Sequence 1635, Ap
16	32	100.0	1688	16	US-10-408-765A-2699	Sequence 2699, Ap
17	30	93.8	15	13	US-10-085-027-3	Sequence 3, Appli
18	30	93.8	66	14	US-10-286-686-6	Sequence 6, Appli
19	30	93.8	81	15	US-10-424-599-262192	Sequence 262192,
20	30	93.8	81	16	US-10-437-963-137779	Sequence 137779,
21	30	93.8	132	16	US-10-767-701-55523	Sequence 55523, A
22	30	93.8	143	9	US-09-779-050A-8	Sequence 8, Appli
23	30	93.8	238	15	US-10-424-599-199169	Sequence 199169,
24	30	93.8	278	15	US-10-449-831A-156	Sequence 156, App
25	30	93.8	279	8	US-08-971-317A-4	Sequence 4, Appli
26	30	93.8	279	9	US-09-193-663-4	Sequence 4, Appli
27	30	93.8	279	10	US-09-873-829-5	Sequence 5, Appli
28	30	93.8	279	13	US-10-017-910-5	Sequence 5, Appli
29	30	93.8	279	15	US-10-279-687-4	Sequence 4, Appli
30	30	93.8	279	15	US-10-662-429-4	Sequence 4, Appli
31	30	93.8	279	15	US-10-662-431-4	Sequence 4, Appli
32	30	93.8	279	15	US-10-662-430-4	Sequence 4, Appli
33	30	93.8	318	15	US-10-449-831A-202	Sequence 202, App
34	30	93.8	399	16	US-10-437-963-158540	Sequence 158540,
35	30	93.8	1231	15	US-10-694-874-3	Sequence 3, Appli
36	30	93.8	1242	9	US-09-903-248-5	Sequence 5, Appli
37	30	93.8	1242	9	US-09-859-604-5	Sequence 5, Appli
38	30	93.8	1242	9	US-09-903-063-5	Sequence 5, Appli
39	30	93.8	1242	9	US-09-903-216-5	Sequence 5, Appli
40	30	93.8	1242	9	US-09-903-199-5	Sequence 5, Appli
41	30	93.8	1242	9	US-09-903-023-5	Sequence 5, Appli
42	30	93.8	1242	10	US-09-436-184-5	Sequence 5, Appli
43	30	93.8	1242	13	US-10-085-027-1	Sequence 1, Appli
44	30	93.8	1242	15	US-10-694-874-1	Sequence 1, Appli
45	30	93.8	1242	16	US-10-735-512-29	Sequence 29, Appli

ALIGNMENTS

RESULT 1
US-10-099-895-4
; Sequence 4, Application US/10099895
; Publication No. US20020177166A1
; GENERAL INFORMATION:
; APPLICANT: BERNDT, Michael C
; APPLICANT: STOMSKI, Frank C
; APPLICANT: LOPEZ, Angel F
; APPLICANT: GUTHRIE, Mark A
; TITLE OF INVENTION: A BINDING MOTIF OF A RECEPTOR
; FILE REFERENCE: 3991/OK379
; CURRENT APPLICATION NUMBER: US/10/099,895
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: PCT/AU00/01118
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-099-895-4

Query Match 100.0% Score 32; DB 13; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY 1 HSRSLP 6
|||||
1 HSRSLP 6

Db 1 HSRSLP 6

RESULT 2
US-10-099-895-31
; Sequence 31, Application US/10099895
; Publication No. US20020177166A1

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/ GENERAL INFORMATION:
/ APPLICANT: BERNDT, Michael C
/ APPLICANT: STOMSKI, Frank C
/ APPLICANT: LOPEZ, Angel F
/ APPLICANT: GUTHRIDGE, Mark A
/ TITLE OF INVENTION: A BINDING MOTIF OF A RECEPTOR
/ FILE REFERENCE: 3991/0K379
/ CURRENT APPLICATION NUMBER: US/10/099,895
/ CURRENT FILING DATE: 2002-03-14
/ PRIOR APPLICATION NUMBER: PCT/AU00/01118
/ PRIOR FILING DATE: 2000-09-15
/ NUMBER OF SEQ ID NOS: 47
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 31
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ OTHER INFORMATION: binding motif of a GM-CSF/IL-3/IL-5 receptor at positions 582 to
/ OTHER INFORMATION: 587
US-10-099-895-31
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Query Match      100.0%; Score 32; DB 13; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 HRSRLP 6
        |||||
Db       1 HRSRLP 6
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RESULT 3
US-10-099-895-35
/ Sequence 35, Application US/1009895
/ Publication No. US20020177166A1
/ GENERAL INFORMATION:
/ APPLICANT: BERNDT, Michael C
/ APPLICANT: STOMSKI, Frank C
/ APPLICANT: LOPEZ, Angel F
/ APPLICANT: GUTHRIDGE, Mark A
/ TITLE OF INVENTION: A BINDING MOTIF OF A RECEPTOR
/ FILE REFERENCE: 3991/0K379
/ CURRENT APPLICATION NUMBER: US/10/099,895
/ CURRENT FILING DATE: 2002-03-14
/ PRIOR APPLICATION NUMBER: PCT/AU00/01118
/ PRIOR FILING DATE: 2000-09-15
/ NUMBER OF SEQ ID NOS: 47
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 35
/ LENGTH: 7
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ OTHER INFORMATION: represents residues 581 to 587
US-10-099-895-35
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```
Query Match      100.0%; Score 32; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HRSRLP 6
        |||||
Db       2 HRSRLP 7
```

```
RESULT 4
US-10-099-895-39
/ Sequence 39, Application US/1009895
/ Publication No. US20020177166A1
/ GENERAL INFORMATION:
/ APPLICANT: BERNDT, Michael C
```

```
/ APPLICANT: STOMSKI, Frank C
/ APPLICANT: LOPEZ, Angel F
/ APPLICANT: GUTHRIDGE, Mark A
/ TITLE OF INVENTION: A BINDING MOTIF OF A RECEPTOR
/ FILE REFERENCE: 3991/0K379
/ CURRENT APPLICATION NUMBER: US/10/099,895
/ CURRENT FILING DATE: 2002-03-14
/ PRIOR APPLICATION NUMBER: PCT/AU00/01118
/ PRIOR FILING DATE: 2000-09-15
/ NUMBER OF SEQ ID NOS: 47
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 39
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-099-895-39
```

```
Query Match      100.0%; Score 32; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HRSRLP 6
        |||||
Db       6 HRSRLP 11
```

```
RESULT 5
US-10-425-114-61894
/ Sequence 61894, Application US/10425114
/ Publication No. US20040034888A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jindong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E
/ APPLICANT: Tabaska, Jack E
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(5313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 61894
/ LENGTH: 142
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: UC-ZMFLMO17206H01_F11.pep
US-10-425-114-61894
```

```
Query Match      100.0%; Score 32; DB 15; Length 142;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HRSRLP 6
        |||||
Db       70 HRSRLP 75
```

```
RESULT 6
US-10-767-701-37000
/ Sequence 37000, Application US/10767701
/ Publication No. US20040172684A1
/ GENERAL INFORMATION:
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(5353)B
/ CURRENT APPLICATION NUMBER: US/10/767,701
/ CURRENT FILING DATE: 2004-01-29
```



```
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 37000
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C13512_1.pep
US-10-767-701-37000
```

```
Query Match          100.0%; Score 32; DB 16; Length 195;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 HSRSLP 6
        |||||
Db       125 HSRSLP 130
```

```
RESULT 7
US-10-437-963-113805
; Sequence 113805, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; TITLE OF INVENTION: L1, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5322)B
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 113805
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) (278)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_17558C.1.pep
US-10-437-963-113805
```

```
Query Match          100.0%; Score 32; DB 16; Length 278;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 HSRSLP 6
        |||||
Db       237 HSRSLP 242
```

```
RESULT 8
US-10-276-774-2338
; Sequence 2338, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21372-030
; CURRENT FILING DATE: 2002-11-18
; CURRENT APPLICATION NUMBER: US/10/276,774
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/496,914
```

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; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2338
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-2338
```

```
Query Match          100.0%; Score 32; DB 15; Length 294;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 HSRSLP 6
        |||||
Db       16 HSRSLP 21
```

```
RESULT 9
US-10-029-386-32140
; Sequence 32140, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: ABOVICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32140
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL133392.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
; OTHER INFORMATION: SWISSPROT HIT: P32927, EVALUE 0.00e+00
US-10-029-386-32140
```

```
Query Match          100.0%; Score 32; DB 14; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 HSRSLP 6
        |||||
Db       75 HSRSLP 80
```

```
RESULT 10
US-10-437-963-117359
; Sequence 117359, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: L1, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
```

```

; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 117359
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_20772C.1.pap
US-10-437-963-117359

Query Match
Best Local Similarity 100.0%; Score 32; DB 16; Length 459;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSRSLP 6
   |||||
Db 389 HSRSLP 394

RESULT 11
US-10-389-566-915
; Sequence 915, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 915
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (27)..(28)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (400)..(400)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; NAME/KEY: misc_feature
; LOCATION: (417)..(417)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-389-566-915

Query Match
Best Local Similarity 100.0%; Score 32; DB 15; Length 471;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSRSLP 6
   |||||
Db 361 HSRSLP 366

RESULT 12
US-10-099-895-1
```

```

; Sequence 1, Application US/10099895
; Publication No. US20020177166A1
; GENERAL INFORMATION:
; APPLICANT: BERNDT, Michael C
; APPLICANT: STOMSKI, Frank C
; APPLICANT: LOPEZ, Angel F
; APPLICANT: GUTHRIE, Mark A
; TITLE OF INVENTION: A BINDING MOTIF OF A RECEPTOR
; FILE REFERENCE: 3991/0K379
; CURRENT APPLICATION NUMBER: US/10/099,895
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: PCT/AU00/01118
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 897
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-099-895-1

Query Match
Best Local Similarity 100.0%; Score 32; DB 13; Length 897;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSRSLP 6
   |||||
Db 598 HSRSLP 603

RESULT 13
US-10-741-600-1633
; Sequence 1633, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO01499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1633
; LENGTH: 897
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1633

Query Match
Best Local Similarity 100.0%; Score 32; DB 17; Length 897;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSRSLP 6
   |||||
Db 598 HSRSLP 603

RESULT 14
US-10-741-600-1634
; Sequence 1634, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO01499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1634
; LENGTH: 897
```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1634

Query Match 100.0%; Score 32; DB 17; Length 897;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HSRSLP 6
Db 598 HSRSLP 603

RESULT 15
US-10-741-600-1635
; Sequence 1635; Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1635
; LENGTH: 903
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1635

Query Match 100.0%; Score 32; DB 17; Length 903;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HSRSLP 6
Db 604 HSRSLP 609

Search completed: March 12, 2005, 09:47:36
Job time : 137 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 09:26:04 ; Search time 40 Seconds
(without alignments)
14,433 Million cell updates/sec

Title: US-10-099-895-4
Perfect score: 32
Sequence: 1 HSRSLP 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	897	1 A39255	cytokine receptor
2	32	100.0	1121	2 S54504	hypothetical prote
3	30	93.8	279	2 A53062	Fas ligand - mouse
4	30	93.8	1231	2 S30185	insulin receptor s
5	30	93.8	1235	1 S16948	insulin receptor s
6	30	93.8	1240	2 JCS209	insulin receptor s
7	30	93.8	1242	2 JCS209	insulin receptor s
8	29	90.6	326	2 AC2953	hypothetical prote
9	29	90.6	326	2 B98330	hypothetical ABC t
10	29	90.6	337	2 G69122	conserved hypothet
11	29	90.6	403	2 AD1254	aspartokinase I (a
12	29	90.6	403	2 AB1617	aspartokinase I (a
13	29	90.6	469	2 S41496	rad22 protein - fl
14	29	90.6	515	2 P88618	protein W06F12.2 l
15	29	90.6	520	2 E97813	WASP, N-WASP, MENA
16	29	90.6	562	2 T26242	hypothetical prote
17	29	90.6	568	2 T26243	hypothetical prote
18	29	90.6	585	2 C49596	genome polypeptide
19	29	90.6	883	2 A96662	hypothetical prote
20	29	90.6	3898	1 A44217	genome polypeptide
21	28	87.5	111	1 KVM540	Ig kappa chain V r
22	28	87.5	111	1 KVM575	Ig kappa chain V r
23	28	87.5	111	1 KVM584	Ig kappa chain V r
24	28	87.5	111	1 KVM585	Ig kappa chain V r
25	28	87.5	112	1 S45715	Ig kappa chain V r
26	28	87.5	144	2 S68454	SRB7 protein homol
27	28	87.5	210	2 A56169	Ig kappa chain V r
28	28	87.5	218	2 S68241	Ig kappa chain V r
29	28	87.5	218	2 JCS810	monoclonal antibod

30	28	87.5	227	2 F36793	hypothetical prote
31	28	87.5	234	2 T35123	SOS response regul
32	28	87.5	248	2 S73606	probable NH(3)-dep
33	28	87.5	288	2 H69170	2-oxoacid-ferredox
34	28	87.5	312	1 S22397	pyruvate synthase
35	28	87.5	312	2 E84268	hypothetical prote
36	28	87.5	316	1 MNVUTV	nonstructural prot
37	28	87.5	524	1 A36205	mitochondrial proc
38	28	87.5	560	2 T23279	hypothetical prote
39	28	87.5	578	2 B71431	hypothetical prote
40	28	87.5	883	2 S31175	hypothetical prote
41	28	87.5	946	2 S54354	inter-alpha-inhibi
42	28	87.5	1026	2 G87346	hypothetical prote
43	28	87.5	3570	2 T45025	mucin MUC5B, trach
44	27	84.4	117	2 H64094	ribosomal protein
45	27	84.4	118	2 C84988	30S ribosomal prot

ALIGNMENTS

RESULT 1
A39255
Cytokine receptor common beta chain precursor - human
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-May-2004
C:Accession: A39255
R:Hayashida, K.; Kitamura, T.; Gorman, D.M.; Arat, K.; Yokota, T.; Miyajima, A.
Proc. Natl. Acad. Sci. U.S.A. 87, 9655-9659, 1990
A:Title: Molecular cloning of a second subunit of the receptor for human granulocyte-mac
A:Reference number: A39255; MUID:91088571; PMID:1702217
A:Accession: A39255
A:Molecule type: mRNA
A:Residues: 1-897 <RAY>
A:Cross-references: GB:M8275
C:Comment: The human high-affinity IL-3, IL-5, and GM-CSF receptors have ligand-specific
C:Genetics:
A:Gene: GDB:CSF2RB
A:Cross-references: GDB:126838; OMIM:138981
A:Map position: 22q13.1-22q13.1
C:Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor h
C:Keywords: alternative splicing; cytokine receptor; duplication; transmembrane protein
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-897/Product: cytokine receptor common beta chain #status predicted <INT>
F:17-443/Domain: extracellular #status predicted <EXT>
F:35-232/Domain: cytokine receptor homology <CRS1>
F:250-431/Domain: cytokine receptor homology <CRS2>
F:444-460/Domain: transmembrane #status predicted <TMM>
F:461-897/Domain: intracellular #status predicted <INT>

Query Match 100.0%; Score 32; DB 1; Length 897;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSRSLP 6
DB 598 HSRSLP 603

RESULT 2
S54504
hypothetical protein YPR030W - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein Y9367.10
C:Species: Saccharomyces cerevisiae
C>Date: 08-Jul-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C:Accession: S54504
R:Badcock, K.; Churcher, C.M.
submitted to the EMBL Data Library, May 1995
A:Reference number: S54059
A:Accession: S54504
A:Molecule type: DNA
A:Residues: 1-1121 <BAD>
A:Cross-references: UNIPROT:Q12734; EMBL:249274; NID:g809585; PID:g809595; MIPS:YPR030W

A:Experimental source: strain AB972
C:Gene: SGD:CSR2
A:Cross-references: SGD:S0006234
A:Map position: 16R

Query Match 100.0%; Score 32; DB 2; Length 1121;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSRSLP 6
DB 337 HSRSLP 342

RESULT 3

A:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: A53062
R:Tabashnik, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nag
Cell 76, 969-976, 1994
A:Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in
A:Accession: A53062; MUID:94185175; PMID:7511063
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-279 <TRAK>
A:Cross-references: UNIPROT:P41047; GB:U06948; NID:G473564; PIDN:AAA17800.1; PID:G473565

Query Match 93.8%; Score 30; DB 2; Length 279;
Best Local Similarity 83.3%; Pred. No. 25;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSRSLP 6
DB 152 HSRSLP 157

RESULT 4

A:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S30185; S43514
R:Keller, S.R.; Aebersold, R.; Garner, C.W.; Lienhard, G.E.
Biochim. Biophys. Acta 1172, 323-326, 1993
A:Title: The insulin-elicited 160 kDa phosphotyrosine protein in mouse adipocytes is an
A:Reference number: S30185; MUID:93192326; PMID:8448209
A:Accession: S30185
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1231 <KEI>
A:Cross-references: UNIPROT:P35569; EMBL:X69722; NID:G297913; PIDN:CAA49378.1; PID:G2979
R:Araki, E.; Haeg, H.; Kahn, C.R.
Biochim. Biophys. Acta 1221, 353-356, 1994
A:Title: Cloning of the mouse insulin receptor substrate-1 (IRS-1) gene and complete seq
A:Reference number: S43514; MUID:94220494; PMID:8167159
A:Accession: S43514
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1037, 'AS', 1038-1179, 'H', 1181-1231 <ARA>
A:Cross-references: EMBL:L24563; NID:G407993; PIDN:AAA9335.1; PID:G407994
C:Superfamily: insulin receptor substrate IRS-1, pleckstrin repeat homology
F,11-113/Domain: pleckstrin repeat homology <PLK>

Query Match 93.8%; Score 30; DB 2; Length 1231;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSRSLP 6

DB 366 HSRSLP 371

RESULT 5

A:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S16948; A39811
R:Sun, X.J.; Rothenberg, P.; Kahn, C.R.; Backer, J.M.; Araki, E.; Wilden, P.A.; Cahill,
Nature 352, 73-77, 1991
A:Title: Structure of the insulin receptor substrate IRS-1 defines a unique signal trans
A:Reference number: S16948; MUID:91287824; PMID:1648180
A:Accession: S16948
A:Molecule type: mRNA
A:Residues: 1-1235 <SUN>
A:Cross-references: UNIPROT:P35570; EMBL:X58375; NID:G56503; PIDN:CAA41264.1; PID:G56504
R:Rothenberg, P.L.; Lane, M.S.; Karasik, A.; Backer, J.; White, M.; Kahn, C.R.
J. Biol. Chem. 266, 8302-8311, 1991
A:Title: Purification and partial sequence analysis of p185, the major cellular substra
A:Reference number: A39811; MUID:91217066; PMID:2022647
A:Accession: A39811
A:Molecule type: protein
A:Residues: 44-51,173-178;223-243;489-506;635-646;671-882, 'I', 884, 'X', 886-888;932-936, 'X
A:Note: the phosphotyrosine residue was not identified
C:Comment: This protein and the beta chain of the insulin receptor itself are the major
C:Comment: phosphorylation of this protein in response to insulin is maximal at 30 secon
insulin.
C:Superfamily: insulin receptor substrate IRS-1; pleckstrin repeat homology
C:Keywords: phosphoprotein; signal transduction
F,11-113/Domain: pleckstrin repeat homology <PLK>
F,872-891/Region: glutamine-rich

Query Match 93.8%; Score 30; DB 1; Length 1235;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSRSLP 6
DB 366 HSRSLP 371

RESULT 6

A:Species: Gallus gallus (chicken)
C:Date: 20-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C:Accession: J05209; PC4305
R:Taouis, M.; Taylor, S.I.; Reisman, M.
Gene 178, 51-55, 1996
A:Title: Cloning of the chicken insulin receptor substrate 1 gene.
A:Reference number: J05209; MUID:97080546; PMID:8921891
A:Accession: J05209
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-1240 <TAO>
A:Cross-references: UNIPROT:P79773; GB:U43502; NID:G1685084; PIDN:AAC60050.1; PID:G16850
A:Accession: PC4305
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <TA2>
C:Comment: This protein acts as a docking protein and mediates multiple interactions amo
C:Gene: Iar-1
A:Gene: Iar-1
C:Superfamily: insulin receptor substrate IRS-1, pleckstrin repeat homology
C:Keywords: phosphoprotein
F,11-112/Domain: pleckstrin repeat homology <PLK>
F,463,549,610,630,660,730,940,987,1010/Binding site: phosphate (Tyr) (covalent) #status

Query Match 93.8%; Score 30; DB 2; Length 1240;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSRSLP 6
 |||||
 Db 369 HSRSLP 374

RESULT 7
 JS0670
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1992 #sequence_revision 23-Aug-1996 #text_change 09-Jul-2004
 C:Accession: JS1160; JS0670; PNO678
 R:Ataki, E.; Sun, X.J.; Haag, B.L.; Chuang, L.; Zhang, Y.; Yang-Feng, T.L.; White, M.; K
 Diabates 42, 1041-1054, 1993
 A:Title: Human skeletal muscle insulin receptor substrate-1. Characterization of the cDN
 A:Reference number: JS1160; MUID:93292738; PMID:8513871
 A:Accession: JS1160
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1242 <RSS>
 A:Cross-references: UNIPROT:P35568; GB:S62539; NID:9386256; PIDN:AA827175.1; PID:9386257
 R:Nishiyama, M.; Wanda, J.R.
 Biochem. Biophys. Res. Commun. 183, 280-285, 1992
 A:Title: Cloning and increased expression of an insulin receptor substrate-1-like gene
 A:Reference number: JS0670; MUID:92181456; PMID:1311924
 A:Accession: JS0670
 A:Molecule type: mRNA
 A:Residues: 1-134, 'G', 135-361, 'R', 363-383, 'R', 385-1242 <NIS>
 A:Cross-references: GB:S85963; NID:9246465; PIDN:AA81608.1; PID:9246466
 A:Experimental source: hepatocellular carcinoma cell line FOCUS
 R:Smith, L.R.; Bradshaw, M.; Croall, D.E.; Garner, C.W.
 Biochem. Biophys. Res. Commun. 196, 767-772, 1993
 A:Title: The insulin receptor substrate (IRS-1) is a PEST protein that is susceptible to
 A:Reference number: PNO678; MUID:94059102; PMID:8240352
 A:Accession: PNO678
 A:Molecule type: protein
 A:Residues: 1-14; 318-353; 411-439; 538-545, 'V', 547-567; 656-697; 724-758; 932-943; 1028-1056; 1
 C:Comment: This protein appears to be the major substrate for insulin-stimulated tyrosin
 o dock various protein containing the phosphotyrosine-binding Src-homology domain 2 (SH
 C:Comment: This protein contains at least 11 PEST regions, which suggests rapid turnover
 C:Genetics:
 A:Gene: GDB:IRSI
 A:Cross-references: GDB:133974; OMIM:147545
 A:Map position: 2q36-q36
 A:Introns: #status absent
 C:Superfamily: Insulin receptor substrate IRS-1; pleckstrin repeat homology
 C:KeyWords: ATP; phosphoprotein
 F:11-113/Domain: pleckstrin repeat homology <PLK>
 F:46, 465-551, 612-662, 732, 941, 989, 1012/Binding site: phosphate (Tyr) (covalent) #stat
 F:78, 527, 1100, 1223/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #
 F:161/Binding site: ATP (Lys) #status predicted
 F:189, 323, 441, 624, 636, 795, 920, 984, 1084, 1218/Binding site: phosphate (Ser) (covalent) (by
 F:300, 351, 774/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status pre

Query Match 93.8%; Score 30; DB 2; Length 1242;
 Best Local Similarity 83.3%; Pred. No. 12e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSRSLP 6
 |||||
 Db 371 HSRSLP 376

RESULT 8
 AC2953
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C:Accession: AC2953
 R:Wood, D.W.; Secubal, J.C.; Kaul, R.; Monks, D.; Chan, L.; Wood, G.E.; Chen, Y.; Woo, L
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuyavin, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; MUID:21608550; PMID:11743193
 A:Accession: AC2953
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-326 <KUR>
 A:Cross-references: UNIPROT:Q8UWZ2; GB:AE008689; PIDN:AAL44041.1; PID:917741603; GSPDB:(
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atu3225
 A:Map position: linear chromosome
 C:Superfamily: 1-arabinose transport system permease araH

Query Match 90.6%; Score 29; DB 2; Length 326;
 Best Local Similarity 83.3%; Pred. No. 50;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSRSLP 6
 |||||
 Db 3 HSRSLP 8

RESULT 9
 B98330
 C:Species: Agrobacterium tumefaciens
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C:Accession: B98330
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldman,
 A.; Liu, F.; Wollm, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.
 Science 294, 2333-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A:Reference number: A97359; MUID:21608551; PMID:11743194
 A:Accession: B98330
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-326 <KUR>
 A:Cross-references: UNIPROT:Q8UWZ2; GB:AE007870; PIDN:AAK90164.1; PID:915160165; GSPDB:(
 C:Genetics:
 A:Gene: AGR_L_3179
 A:Map position: linear chromosome
 C:Superfamily: 1-arabinose transport system permease araH

Query Match 90.6%; Score 29; DB 2; Length 326;
 Best Local Similarity 83.3%; Pred. No. 50;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSRSLP 6
 |||||
 Db 3 HSRSLP 8

RESULT 10
 G69122
 C:Species: Agrobacterium tumefaciens
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C:Accession: G69122
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
 K.S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func
 A:Reference number: A69000; MUID:98037514; PMID:9371463
 A:Accession: G69122
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-337 <MTH>
 A:Cross-references: UNIPROT:Q27937; GB:AE000942; GB:AE000666; NID:92623039; PIDN:AA8063;
 A:Experimental source: strain Delta H
 C:Genetics:

A:Gene: MTH1915
A:Start codon: GTG
C:Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0025

Query Match 90.6%; Score 29; DB 2; Length 337;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSRSLP 6
|||:|
Db 191 HSRNLP 196

RESULT 11

AD1254
Aspartokinase I (alpha and beta chains) homolog lmo1436 (imported) - Listeria monocytogenes
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 16-Aug-2004
C:Accession: AD1254

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Feihl, H. Science 294, 849-852, 2001
A:Authors: Krefte, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluerer, T.; Simoes, N.; Tietz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AD1254
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-403 <GLA>
A:Cross-references: UNIPROT:Q8765; GB:NC_003210; PIDN:CAC99514.1; PID:G16410865; GSPDB:A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo1436
C:Superfamily: Aspartate kinase; aspartate kinase homology

Query Match 90.6%; Score 29; DB 2; Length 403;
Best Local Similarity 83.3%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSRSLP 6
|||:|
Db 193 HARSLP 198

RESULT 12

AB1617
Aspartokinase I (alpha and beta chains) homolog lin1475 (imported) - Listeria innocua (S
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 16-Aug-2004
C:Accession: AB1617

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Feihl, H.; Science 294, 849-852, 2001
A:Authors: Krefte, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluerer, T.; Simoes, N.; Tietz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AB1617
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-403 <GLA>
A:Cross-references: UNIPROT:Q92BR9; GB:AL592022; PIDN:CAC96706.1; PID:G16413948; GSPDB:A:Experimental source: strain C11p11262
C:Genetics:
A:Gene: lin1475
C:Superfamily: Aspartate kinase; aspartate kinase homology

Query Match 90.6%; Score 29; DB 2; Length 403;
Best Local Similarity 83.3%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSRSLP 6
|||:|
Db 193 HARSLP 198

RESULT 13

S41496
rad22 protein - fission yeast (Schizosaccharomyces pombe)
N:Alternate names: protein SPAC30D11.10; RAD52 protein homolog
C:Species: Schizosaccharomyces pombe
C:Date: 18-May-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S41496; I38589; S37033; S62568
R:Ostermann, K.; Lorentz, A.; Schmidt, H. Nucleic Acids Res. 21, 5940-5944, 1993
A:Title: The fission yeast rad22 gene, having a function in mating-type switching and re
A:Reference number: S41496; MUID:94119694; PMID:8250356
A:Accession: S41496
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-469 <OST>
A:Cross-references: UNIPROT:P36592; EMBL:X72220; NID:G397582; PIDN:CAA51021.1; PID:G3975
R:Pearson, D.; Churcher, C.M.; Barrett, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, November 1995
A:Reference number: Z21801
A:Accession: J38589
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-33,'T',85-469 <PE2>
A:Cross-references: EMBL:Z67961; NID:G1065887; PIDN:CAA91896.1; PID:G1065897; GSPDB:GNO0
A:Experimental source: strain 972h-; cosmid c30D11
C:Genetics:
A:Gene: rad22; SPAC30D11.10
A:Map position: 1L

Query Match 90.6%; Score 29; DB 2; Length 469;
Best Local Similarity 83.3%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSRSLP 6
|||:|
Db 376 HRSKSLP 381

RESULT 14

F88618
Protein W06F12.2 (imported) - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: F88618
R:anonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websties genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Accession: F88618
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-515 <STO>
A:Cross-references: UNIPROT:Q9U345; GB:chr_III; PIDN:CAB05828.1; PID:G3880554; GSPDB:GNO
C:Genetics:
A:Gene: W06F12.2
A:Map position: 3

Query Match 90.6%; Score 29; DB 2; Length 515;
Best Local Similarity 83.3%; Pred. No. 80;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSRSLP 6
|||:|
Db 259 HRSRVP 264

RESULT 15

E97813
WASP, N-WASP, MENA proteins homolog [imported] - Rickettsia conorii (strain Malish 7)
C:Species: Rickettsia conorii
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: E97813
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A:Reference number: A97700; MUID:21442074; PMID:11557893
A:Accession: E97813
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-520 <KUR>
A:Cross-references: UNIPROT:Q92H62; GB:AE006914; PIDN:AAL03447.1; PID:G15620016; GSPDB:G
C:Gene: RC0909

Query Match 90.6%; Score 29; DB 2; Length 520;
Best Local Similarity 83.3%; Pred.No. 81;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSRSLP 6
|:||||
Db 55 HNRSLP 60

Search completed: March 12, 2005, 09:35:35
Job time : 41 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 09:17:49 ; Search time 176 Seconds
(without alignments)
17.457 Million cell updates/sec

Title: US-10-099-895-4
Perfect score: 32
Sequence: 1 HSRSLP 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	157	2	0871Y2
2	32	100.0	156	2	06ZUC0
3	32	100.0	226	2	06BP48
4	32	100.0	291	2	08WMC4
5	32	100.0	291	2	09H671
6	32	100.0	331	2	08GZB3
7	32	100.0	425	2	06Z8C7
8	32	100.0	459	2	06Z8C8
9	32	100.0	466	2	095B59
10	32	100.0	466	2	095B60
11	32	100.0	466	2	095B63
12	32	100.0	466	2	095B64
13	32	100.0	466	2	095B65
14	32	100.0	499	1	MATK_LEPPR
15	32	100.0	499	2	08MEX6
16	32	100.0	499	2	08MEX7
17	32	100.0	505	2	08MEX9
18	32	100.0	507	2	08WDS8
19	32	100.0	514	1	MATK_ZAMFL
20	32	100.0	514	1	MATK_ZAMFL
21	32	100.0	827	2	06GQJ2
22	32	100.0	889	2	06NSJ8
23	32	100.0	897	1	CYRB_HUMAN
24	32	100.0	903	2	06ICE0
25	32	100.0	1121	2	01Z734
26	30	93.8	279	1	TNR6_MOUSE
27	30	93.8	279	1	07TMV9
28	30	93.8	289	2	08BN58
29	30	93.8	399	2	06K4B7
30	30	93.8	885	2	091615
31	30	93.8	1229	2	066H99

32	30	93.8	1233	1	IRS1_MOUSE	P35569 mus musculus
33	30	93.8	1235	1	IRS1_RAT	P35570 rattus norv
34	30	93.8	1240	2	P79773	P79773 gallus gall
35	30	93.8	1242	1	IRS1_HUMAN	P35568 homo sapien
36	30	93.8	1251	2	Q28224	Q28224 cercopithe
37	29	90.6	117	2	06F526	06F526 bovine vira
38	29	90.6	117	2	06F527	06F527 bovine vira
39	29	90.6	117	2	06F528	06F528 bovine vira
40	29	90.6	117	2	06F529	06F529 bovine vira
41	29	90.6	117	2	06F600	06F600 bovine vira
42	29	90.6	117	2	06F603	06F603 bovine vira
43	29	90.6	117	2	06F604	06F604 bovine vira
44	29	90.6	117	2	06F605	06F605 bovine vira
45	29	90.6	117	2	06F606	06F606 bovine vira

ALIGNMENTS

RESULT 1						
ID	0871Y2	PRELIMINARY:	PRT:	157 AA.		
AC	0871Y2					
DT	01-JUN-2003 (TREMBLrel. 24, Created)					
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)					
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)					
DE	Hypothetical protein B9K17.075.					
GN	Name=B9K17.075;					
OS	Neurospora crassa.					
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;					
OC	Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.					
OX	NCBI_TaxId=5141;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	Schulte U., Aign V., Hohlseil J., Brandt P., Fartmann B., Holland R.,					
RA	Nyakatura G., Mewes H.W., Mannhaupt G.;					
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.					
RP	[2]					
RA	SEQUENCE FROM N.A.					
RA	German Neurospora genome project;					
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.					
DR	EMBL; BX294016; CAD70853.1; -					
DR	InterPro; IPR000345; CYC_heme_BS.					
DR	InterPro; IPR003066; IG_MHC.					
DR	PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.					
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.					
KW	Hypothetical protein.					
SQ	SEQUENCE 157 AA; 17596 MW; 91706CEAE30B62E CRC64;					
Query Match						
			100.0%;	Score 32;	DB 2;	Length 157;
			Best Local Similarity	100.0%;	Pred. NO. 25;	
			Matches 6;	Conservative	0;	Mismatches 0;
					Indels 0;	Gaps 0;
Oy	1 HSRSLP 6					
Db	148 HSRSLP 153					
RESULT 2						
ID	06ZUC0	PRELIMINARY:	PRT:	166 AA.		
AC	06ZUC0					
DT	05-JUL-2004 (TREMBLrel. 27, Created)					
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)					
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)					
DE	Hypothetical protein FLJ43828.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
OX	NCBI_TaxId=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Testis;					

RA Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Sugiyama T.,
 RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
 RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
 RA Yamashta H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
 RA Magatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Ohnima A.,
 RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
 RA Masuno Y., Nagai K., Isogai T.,
 RA Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK125816; BAC6305.1; -.
 SO SEQUENCE 166 AA; 17738 MW; ED8C12B80E6D5579 CRC64;

Query Match 100.0%; Score 32; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSRSLP 6
 |||||
 Db 30 HSRSLP 35

RESULT 3

Q6BP48 PRELIMINARY; PRT; 226 AA.
 AC O6BP48;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Similar to CA3513|IPF11246 Candida albicans IPF11246 unknown
 DE function.
 GN ORFNames=DEHA0E172599;
 OS Debaryomyces hansenii CBS767.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes;
 OX NCBI_TaxID=284592;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS767;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anhouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Bolstrame A., Boyer J., Catolico L., Confantieri F., de Darvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantave F., Hennequin C., Janniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Keszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Niclaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Galliard C., Weissenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS767;
 RG Genoscope;
 RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR382137; CAG88275.1; -.
 DR InterPro; IPR006973; CwF_CwC_15.
 DR Pfam; PF04889; CwF_CwC_15; 1.
 SO SEQUENCE 226 AA; 26224 MW; E0F399D576D3DC9 CRC64;

Query Match 100.0%; Score 32; DB 2; Length 226;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSRSLP 6
 |||||
 Db 25 HSRSLP 30

RESULT 4
 Q8WMC4 PRELIMINARY; PRT; 291 AA.
 AC Q8WMC4;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein FLJ22555.
 GN Name=FLJ22555;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loughlano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bogak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerk A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC017959; AAH17959.1; -.
 KW Hypothetical protein.
 SO SEQUENCE 291 AA; 32544 MW; 97D958B2AC9C1163 CRC64;

Query Match 100.0%; Score 32; DB 2; Length 291;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSRSLP 6
 |||||
 Db 13 HSRSLP 18

RESULT 5

Q9H671 PRELIMINARY; PRT; 291 AA.
 AC Q9H671;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein FLJ22555.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human small intestine;
 RA Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
 RA Suzuki Y., Ohtsuka M., Nishii T., Shibahara T., Tanaka T.,
 RA Nakamura Y., Isogai T., Sugano S.;

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK026208; BAB15393.1; -.
 SQ SEQUENCE 291 AA; 32486 MW; 04EA58B0C61830C CRC64;

Query Match 100.0%; Score 32; DB 2; Length 291;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HSRSLP 6
 |||||
 Db 13 HSRSLP 18

RESULT 6

O6GZB3 PRELIMINARY; PRT; 331 AA.

AC O6GZB3; (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE PABA (Fragment).
 OS Xerophyta humilis.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Velloziaceae; Xerophyta.
 OX NCBI_TaxID=211604;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22928317; PubMed=12966044;
 RA Collett H., Butow R., Smith J., Farrant J., Illing N.;
 RT "Photosynthetic genes are differentially transcribed during the
 RT dehydration-rehydration cycle in the resurrection plant, Xerophyta
 RT humilis".
 RL J. Exp. Bot. 54:2593-2595(2003).

DR EMBL: AF545583; AAN77239.1; -.
 DR GO: GO:0030077; C:light-harvesting complex (sensu Proteobacte. . .; IEA.
 DR GO: GO:0045156; F:electron transporter, transferring electron. . .; IEA.
 DR GO: GO:0006118; F:electron transport; IEA.
 DR GO: GO:0019684; P:photosynthesis, light reaction; IEA.
 DR InterPro; IPR005867; Photo_DI.
 DR InterPro; IPR00484; Photo_RC.
 DR Pfam; PF00124; Photo_RC.1.
 DR PRINTS; PR00256; REACTCENTRE.
 DR ProDom; PD000551; Photo_RC.1.
 DR TIGRfam; TIGR01151; pBDA.1.
 DR PROSITE; PS00244; REACTON_CENTER; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 331
 SQ SEQUENCE 331 AA; 35965 MW; CBC6A00364E67D2D CRC64;

Query Match 100.0%; Score 32; DB 2; Length 331;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HSRSLP 6
 |||||
 Db 266 HSRSLP 271

RESULT 7

O6Z8C7 PRELIMINARY; PRT; 425 AA.

AC O6Z8C7; (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Putative serine/threonine-protein kinase Mak.
 GN Name=P0459B01.42-2; Synonyms=OJ1111 E07.13-2;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriaridaceae; Oryzae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL: AP004778; BAD07892.1; -.
 DR EMBL: AP003994; BAD07521.1; -.

DR HSP; P24941; IKE8.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR01009; Kinase_like.
 DR InterPro; IPR00719; Prot_Kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR008371; Ser_thr_pkin_AS.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; Pkinase.1.
 DR ProDom; PD000001; Prot_Kinase.1.
 DR SMART; SM00220; S_TKc.1.
 DR SMART; SM00219; TYKc.1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM.1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST.1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 425 AA; 47898 MW; 005CFD20336DB95 CRC64;

Query Match 100.0%; Score 32; DB 2; Length 425;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HSRSLP 6
 |||||
 Db 355 HSRSLP 360

RESULT 8

O6Z8C8 PRELIMINARY; PRT; 459 AA.

AC O6Z8C8; (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Putative serine/threonine-protein kinase Mak.
 GN Name=P0459B01.42-1; Synonyms=OJ1111 E07.13-1;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriaridaceae; Oryzae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL: AP004778; BAD07891.1; -.
 DR EMBL: AP003994; BAD07520.1; -.
 DR HSP; P24941; IKB8.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR01009; Kinase_like.
 DR InterPro; IPR000719; Prot_Kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.

DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TYKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 459 AA; 51720 MW; B527BD7C8B1551F CRC64;

Query Match
Best Local Similarity 100.0%; Score 32; DB 2; Length 459;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSRSLP 6
|||||
Db 389 HSRSLP 394

RESULT 9
ID Q95B59 PRELIMINARY; PRT; 466 AA.
AC Q95B59;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Mack (Fragment).
GN Name=mack;
OS Bowenia serrulata (Byfield cycad).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Cycadophyta; Cycadales; Cycadaceae; Bowenia.
OX NCBI_TaxID=13365;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang S., Wang D., Yu X.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410173; AL10204.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0008380; P:RNA splicing; IEA.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; Mack_N_maturase2.
DR Pfam; PF01348; Intron_maturase2; 1.
DR Pfam; PF01824; Mack_N; 1.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 466 AA; 55467 MW; 585470BC737B6360 CRC64;

Query Match
Best Local Similarity 100.0%; Score 32; DB 2; Length 466;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSRSLP 6
|||||
Db 232 HSRSLP 237

RESULT 10
ID Q95B60 PRELIMINARY; PRT; 466 AA.
AC Q95B60;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Mack (Fragment).
GN Name=mack;
OS Ceratozamia hildea (Bamboo cycad).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Cycadophyta; Cycadales; Zamiales; Ceratozamia.
OX NCBI_TaxID=171009;

RN [1]
RP SEQUENCE FROM N.A.
RA Zhang S., Wang D., Yu X.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410172; AL10203.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0008380; P:RNA splicing; IEA.
DR InterPro; IPR008998; Agglutinin.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; Mack_N_maturase2.
DR Pfam; PF01348; Intron_maturase2; 1.
DR Pfam; PF01824; Mack_N; 1.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 466 AA; 55603 MW; A98B324FB0C62AF0 CRC64;

Query Match
Best Local Similarity 100.0%; Score 32; DB 2; Length 466;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSRSLP 6
|||||
Db 232 HSRSLP 237

RESULT 11
ID Q95B63 PRELIMINARY; PRT; 466 AA.
AC Q95B63;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Mack (Fragment).
GN Name=mack;
OS Eucephalartos horridus (Ferocious blue cycad).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Cycadophyta; Cycadales; Zamiales; Eucephalartos.
OX NCBI_TaxID=171018;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang S., Wang D., Yu X.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410169; AL10200.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0008380; P:RNA splicing; IEA.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; Mack_N_maturase2.
DR Pfam; PF01348; Intron_maturase2; 1.
DR Pfam; PF01824; Mack_N; 1.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 466 AA; 55504 MW; 0251B969318B88F8 CRC64;

Query Match
Best Local Similarity 100.0%; Score 32; DB 2; Length 466;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSRSLP 6
|||||
Db 232 HSRSLP 237

RESULT 12
ID Q95B64 PRELIMINARY; PRT; 466 AA.
AC Q95B64;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Mack (Fragment).
GN Name=mack;
OS Macrozamia dyeri.

```
OG Chloroplast.
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Cycadophyta; Cycadales; Zamiaceae; Macrozamia.
OX NCBI_TaxId=171019;
RN
RP SEQUENCE FROM N.A.
RA Zhang S., Wang D., Yu X.;
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF410167; AAL10199.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
DR InterPro; IPR000442; Intron_maturase2.
DR Pfam; PF01348; Intron_maturase2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 466 AA; 55286 MW; 801840904CBF133A CRC64;

Query Match
Best Local Similarity 100.0%; Score 32; DB 2; Length 466;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSRSLP 6
DB 232 HSRSLP 237

RESULT 13
OG 095B65 PRELIMINARY; PRT; 466 AA.
AC 095B65;
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE MatK (Fragment).
GN Name=matk;
OS Lepidozamia peroffekyana (Scaly zamia).
OC Chloroplast.
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Cycadophyta; Cycadales; Zamiaceae; Lepidozamia.
OX NCBI_TaxId=133430;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang S., Wang D., Yu X.;
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF410167; AAL10199.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N; 1.
DR Pfam; PF01348; Intron_maturase2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 466 AA; 55286 MW; E1C34F9767A438F0 CRC64;

Query Match
Best Local Similarity 100.0%; Score 32; DB 2; Length 466;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSRSLP 6
DB 232 HSRSLP 237

RESULT 14
MATK CERME STANDARD; PRT; 499 AA.
AC Q8MEY4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
```

```
DE Maturase K (Intron maturase).
GN Name=matk;
OS Ceratozamia mexicana (Mexican horncone).
OG Chloroplast.
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Cycadophyta; Cycadales; Zamiaceae; Ceratozamia.
OX NCBI_TaxId=41994;
RN [1]
RP SEQUENCE FROM N.A.
RA Chaw S.-M., Hu S.-H.;
RT "Chloroplast matk sequence data reconfirm the monophyly of extant
RT gymnosperms and the coniferophytic origin of Getales.";
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
CC -!- FUNCTION: Probably assists in splicing chloroplast group II
CC introns (By similarity).
CC -!- SIMILARITY: Belongs to the intron maturase family 2. Matk
CC subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF279794; AAK69117.1; -.
DR InterPro; IPR008998; Agglutinin.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturase2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW Chloroplast; mRNA processing.
SQ SEQUENCE 499 AA; 59648 MW; 2127CADAFCC397DE CRC64;

Query Match
Best Local Similarity 100.0%; Score 32; DB 1; Length 499;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSRSLP 6
DB 232 HSRSLP 237

RESULT 15
OG 08MEX6 PRELIMINARY; PRT; 499 AA.
AC 08MEX6;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Maturase K.
GN Name=matk;
OS Macrozamia moorei.
OG Chloroplast.
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Cycadophyta; Cycadales; Zamiaceae; Macrozamia.
OX NCBI_TaxId=133431;
RN [1]
RP SEQUENCE FROM N.A.
RA Chaw S.-M., Hu S.-H.;
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF279802; AAK69125.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0008380; P:RNA splicing; IEA.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturase2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW Chloroplast.
SQ SEQUENCE 499 AA; 59312 MW; E3B7321EB392CCB CRC64;

Query Match
Best Local Similarity 100.0%; Score 32; DB 2; Length 499;
```

Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSRSLP 6
|||
Db 232 HSRSLP 237

Search completed: March 12, 2005, 09:34:50
Job time : 178 secs